

Amendments to the Specification:

Amend the paragraph beginning at page 1, line 3, as follows.

Cross Reference to Related Applications

This application is a continuation of U.S. Patent Application Serial Number 10/039,112, filed December 31, 2001, which, in turn, is a continuation of U.S. Patent Application Serial Number 09/650,324, filed August 29, 2000, now U.S. Patent Number 6,638,720, which, in turn, is a continuation of U.S. Patent Application Serial Number 09/579,259, filed May 25, 2000, now U.S. Patent Number 6,558,953, which, in turn, is a continuation of U.S. Patent Application Serial Number 09/224,898, filed December 31, 1998, now abandoned, which, in turn, is a divisional of U.S. Patent Application Serial Number 08/770,544, filed December 20, 1996, now U.S. Patent Number 5,907,085, which claims the benefit of U.S. Provisional Patent Application Serial Number 60/009,008, filed December 21, 1995.

Replace the paragraph beginning at page 10, line 14, with the following paragraph.

Figure 2 shows the nucleotide (SEQ ID NO:7) and amino acid (SEQ ID NO:8) sequences of a PCR amplified fragment of the GLRaV-3 genome. The external and internal primers used for PCR are underlined and their orientations are indicated by arrows.

Replace the paragraph beginning at page 10, line 19, with the following paragraph.

Figure 3 compares the alignment of the amino acid sequence deduced from the PCR fragment of GLRaV-3 (SEQ ID NO:8) with respective regions of HSP90 homologues of beet yellow virus (“BYV”) (p64) (SEQ ID NO:33), citrus tristeza virus (“CTV”) (p61) (SEQ ID NO:34), and lettuce infectious yellow virus (“LIYV”) (p59) (SEQ ID NO:35). Consensus amino acid residues are shown. Uppercase letters indicate identical amino acids, lowercase letters indicate at least three identical or functionally similar amino acids.

Replace the paragraph beginning at page 12, line 3, with the following paragraph.

Figure 10 shows the nucleotide (SEQ ID NO:9) and amino acid (SEQ ID NO:10) sequences of the coat protein of grapevine leafroll associated closterovirus-3, isolate NY1. Nucleotide sequencing was conducted by the procedure described in Example 1. The translated amino acid sequence is shown below the nucleotide sequence.

Replace the paragraph beginning at page 12, line 9, with the following paragraph.

Figure 11 compares the alignment of the coat protein of GLRaV-3 (SEQ ID NO:10) with respect to BYV (SEQ ID NO:36), CTV (SEQ ID NO:37), and LIYV (SEQ ID NO:38). Consensus amino acid residues are shown. Uppercase letters indicate identical amino acids, and lowercase letters indicate at least three identical or functionally similar amino acids. The three conserved amino acid residues (S, R, and D) identified in all filamentous plant virus coat proteins are in bold (Dolja et al., “Phylogeny of Capsid Proteins of Rod-shaped and Filamentous RNA Plant Viruses: Two Families with Distinct Patterns of Sequence and Probably Structure Conservation,” Virology, 184:79-86 (1991)).

Replace the paragraph beginning at page 15, line 1, with the following paragraph.

Figures 18 A to W show the nucleotide sequence and partial genome organization of GLRaV-3 (SEQ ID NOS:1-24 and 39-48).

Replace the paragraph beginning at page 15, line 12, with the following paragraph.

Figure 20 compares the amino acid sequence alignment of the helicase of GLRaV-3 (SEQ ID NO:2) with respect to BYV (SEQ ID NO:49), CTV (SEQ ID NO:50), and LIYV (SEQ ID NO:51). Consensus amino acid residues are shown. Uppercase letters indicate identical amino acids, lowercase letters indicate at least three identical or functionally similar amino acids. Six conserved motifs (I to VI) that are conserved among the Superfamily 1 helicase (Koonin et al., “Evolution and Taxonomy of Positive-strand RNA Viruses: Implications of Comparative Analysis of Amino Acid Sequences,” Critical Reviews in Biochemistry and Molecular Biology, 28:375-430 (1993)) of the positive-strand RNA viruses are overlined.

Replace the paragraph beginning at page 16, line 8, with the following paragraph.

Figure 22 compares the amino acid sequence alignment of the RNA dependent RNA polymerase (RdRp) of GLRaV-3 (SEQ ID NO:4) with respect to BYV (SEQ ID NO:52), CTV (SEQ ID NO:53), and LIYV (SEQ ID NO:54). Consensus amino acid residues are shown. Uppercase letters indicate identical amino acids, and lower case letters indicate at least three identical or functionally similar amino acids. The motifs (I to VIII) that are conserved among Supergroup 3 RNA polymerase of positive-strand RNA viruses are overlined.

Replace the paragraph beginning at page 16, line 34, with the following paragraph.

Figure 24 compares the alignment of the GLRaV-3 and LIYV nucleotide sequences (presented as DNA) in the vicinity of the proposed frameshift, nt 4,099-4,165 in GLRaV-3 (SEQ ID NO:1) and nt 5,649-5,715 in LIYV (SEQ ID NO:64). Identical nucleotides are typed in uppercase letters. LIYV +1 frameshift region (aAAG) and the corresponding GLRaV-3 (cACA) are bold and italic. The encoded C-terminus of the HEL and N-terminus of RdRp are presented above (GLRaV-3) (SEQ ID NOS:2 and 4) and below (LIYV) (SEQ ID NOS:65 and 66) the nucleotide alignment. Repeat sequences are underlined.

Replace the paragraph beginning at page 17, line 9, with the following paragraph.

Figure 25 compares the amino acid alignment of the small hydrophobic transmembrane protein of GLRaV-3 p5K (SEQ ID NO:14) with respect to BYV (p6K) (SEQ ID NO:55), CTV (p6K) (SEQ ID NO:57), and LIYV (p5K) (SEQ ID NO:56). Consensus amino acid residues are shown. Lowercase letters indicate at least three identical or functionally similar amino acids. The transmembrane domain that has been identified in several other closteroviruses, BYV, CTV, and LIYV (Karasev et al., “Complete Sequence of the Citrus Tristeza Virus RNA Genome,” Virology, 208:511-520 (1995)), is overlined.

Replace the paragraph beginning at page 17, line 19, with the following paragraph.

Figures 26 A to B present the amino acid sequence alignment of the HSP70-related protein of GLRaV-3 (p59K) (SEQ ID NO:6) with respect to BYV (p65K) (SEQ ID NO:58), CTV (p65K) (SEQ ID NO:59), and LIYV (p62K) (SEQ ID NO:60). The eight conserved motifs (A to H) of cellular HSP70 are overlined. Consensus amino acid residues are shown. Uppercase letters indicate identical amino acids, and lowercase letters indicate at least three identical or functionally similar amino acids.

Replace the paragraph beginning at page 18, line 23, with the following paragraph.

Figures 28 A to B compare the amino acid sequence alignment of the HSP90-related proteins of GLRaV-3 (p55K) (SEQ ID NO:8) with respect to BYV (p64K) (SEQ ID NO:61), CTV (p61K) (SEQ ID NO:62), and LIYV (p59K) (SEQ ID NO:63). Two domains, I and II, which have been identified on CTV (p61K) are overlined. Consensus amino acid residues are shown. Uppercase letters indicate identical amino acids; lowercase letters indicate at least three identical or functionally similar amino acids.

Replace the paragraph beginning at page 18, line 32, with the following paragraph.

Figures 29 A to B show a nucleotide sequence fragment (SEQ ID NOS:1, 7, 29, and 67) containing the 43 kDa open reading frame (SEQ ID NO:8) that was used to engineer a plant expression cassette, pBI525GLRaV-3hsp90. This sequence fragment (from nucleotides 9,404 to 10,503 of the partial GLRaV-3 genome sequence, Figure 18) was later proven to be located in the 3' portion of GLRaV-3 HSP90-related gene. Nucleotides in the lower case were designed to facilitate engineering by addition of NcoI restriction sites.